

## **STIC Biotechnology Systems Branch**

### **RAW SEQUENCE LISTING** **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/ 570,904  
Source: IFWP  
Date Processed by STIC: 3-22-06

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE **CHECKER VERSION 4.4.0 PROGRAM**, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

**<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>**

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<**<http://www.uspto.gov/ebc/efs/downloads/documents.htm>**> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05):  
U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

## Raw Sequence Listing Error Summary

### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 10/570,904

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1      Wrapped Nucleics  
    Wrapped Aminos      The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2      Invalid Line Length      The rules require that a line **not exceed** 72 characters in length. This includes white spaces.
  
- 3      Misaligned Amino  
    Numbering      The numbering under each 5<sup>th</sup> amino acid is misaligned. Do **not** use tab codes between numbers; use **space characters**, instead.
  
- 4      Non-ASCII      The submitted file was **not** saved in ASCII(DOS) text, as **required** by the Sequence Rules. **Please ensure your subsequent submission is saved in ASCII text.**
  
- 5      Variable Length      Sequence(s)      contain n's or Xaa's representing more than one residue. **Per Sequence Rules, each n or Xaa can only represent a single residue.** Please present the **maximum** number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6      PatentIn 2.0  
    "bug"      A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)             . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. **This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.**
  
- 7      Skipped Sequences  
    (OLD RULES)      Sequence(s)      missing. If intentional, please insert the following lines for **each** skipped sequence:  
     (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     (i)      SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
     (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
     This sequence is intentionally skipped  
  
     Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to **include** the skipped sequences.
  
- 8      Skipped Sequences  
    (NEW RULES)      Sequence(s)      missing. If **intentional**, please insert the following lines for **each** skipped sequence.  
     <210> sequence id number  
     <400> sequence id number  
     000
  
- 9      Use of n's or Xaa's  
    (NEW RULES)      Use of n's and/or Xaa's have been detected in the Sequence Listing.  
     Per 1.823 of Sequence Rules, use of <220>-<223> is **MANDATORY** if n's or Xaa's are present.  
     In <220> to <223> section, please explain location of **n** or **Xaa**, and which residue **n** or **Xaa** represents.
  
- 10      Invalid <213>  
    Response      Per 1.823 of Sequence Rules, the only **valid** <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is **required** when <213> response is Unknown or is Artificial Sequence
  
- 11      Use of <220>      Use of <220> to <223> is **MANDATORY** if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
     (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12      PatentIn 2.0  
    "bug"      Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
  
- 13      Misuse of n/Xaa      "n" can **only** represent a single nucleotide; "Xaa" can **only** represent a single amino acid



IFWP

## RAW SEQUENCE LISTING

DATE: 03/22/2006

PATENT APPLICATION: US/10/570,904

TIME: 14:56:03

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

3 <110> APPLICANT: TAKESHIMA, Seiji  
 4 MATSUMURA, Tadanobu  
 5 KISHIMOTO, Takahide  
 6 OKA, Masanori  
 7 HIRAYAMA, Noriaki  
 9 <120> TITLE OF INVENTION: MODIFIED PYRROLOQUINOLINE QUINONE (PQQ) DEPENDENT GLUCOSE  
 DEHYDROGENASE  
 10 EXCELLENT IN SUBSTRATE SPECIFICITY  
 12 <130> FILE REFERENCE: 251134  
 C--> 14 <140> CURRENT APPLICATION NUMBER: US/10/570,904  
 C--> 14 <141> CURRENT FILING DATE: 2006-03-07  
 14 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/012508  
 15 <151> PRIOR FILING DATE: 2004-08-31  
 17 <150> PRIOR APPLICATION NUMBER: JP 2003-315797  
 18 <151> PRIOR FILING DATE: 2003-09-08  
 20 <150> PRIOR APPLICATION NUMBER: JP 2003-315799  
 21 <151> PRIOR FILING DATE: 2003-09-08  
 23 <150> PRIOR APPLICATION NUMBER: JP 2004-060283  
 24 <151> PRIOR FILING DATE: 2004-03-04  
 26 <150> PRIOR APPLICATION NUMBER: JP 2004-060282  
 27 <151> PRIOR FILING DATE: 2004-03-04  
 29 <150> PRIOR APPLICATION NUMBER: JP 2004-151905  
 30 <151> PRIOR FILING DATE: 2004-05-21  
 32 <160> NUMBER OF SEQ ID NOS: 94  
 34 <170> SOFTWARE: PatentIn version 3.1  
 36 <210> SEQ ID NO: 1  
 37 <211> LENGTH: 455  
 38 <212> TYPE: PRT  
 39 <213> ORGANISM: Acinetobacter baumannii  
 41 <400> SEQUENCE: 1  
 43 Asp Ile Pro Leu Thr Pro Ala Gln Phe Ala Lys Ala Lys Thr Glu Asn  
 44 1 5 10 15  
 47 Phe Asp Lys Lys Val Ile Leu Ser Asn Leu Asn Lys Pro His Ala Leu  
 48 20 25 30  
 51 Leu Trp Gly Pro Asp Asn Gln Ile Trp Leu Thr Glu Arg Ala Thr Gly  
 52 35 40 45  
 55 Lys Ile Leu Arg Val Asn Pro Val Ser Gly Ser Ala Lys Thr Val Phe  
 56 50 55 60  
 59 Gln Val Pro Glu Ile Val Ser Asp Ala Asp Gly Gln Asn Gly Leu Leu  
 60 65 70 75 80  
 63 Gly Phe Ala Phe His Pro Asp Phe Lys His Asn Pro Tyr Ile Tyr Ile  
 64 85 90 95  
 67 Ser Gly Thr Phe Lys Asn Pro Lys Ser Thr Asp Lys Glu Leu Pro Asn  
 68 100 105 110

(pg.8)

Does Not Comply  
 Corrected Diskette Needed  
 (pg.6-7) ←

## RAW SEQUENCE LISTING

DATE: 03/22/2006

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TIME: 14:56:03

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

```

71 Gln Thr Ile Ile Arg Arg Tyr Thr Tyr Asn Lys Thr Thr Asp Thr Phe
72      115      120      125
75 Glu Lys Pro Ile Asp Leu Ile Ala Gly Leu Pro Ser Ser Lys Asp His
76      130      135      140
79 Gln Ser Gly Arg Leu Val Ile Gly Pro Asp Gln Lys Ile Tyr Tyr Thr
80 145      150      155      160
83 Ile Gly Asp Gln Gly Arg Asn Gln Leu Ala Tyr Leu Phe Leu Pro Asn
84      165      170      175
87 Gln Ala Gln His Thr Pro Thr Gln Gln Glu Leu Asn Ser Lys Asp Tyr
88      180      185      190
91 His Thr Tyr Met Gly Lys Val Leu Arg Leu Asn Leu Asp Gly Ser Val
92      195      200      205
95 Pro Lys Asp Asn Pro Ser Phe Asn Gly Val Val Ser His Ile Tyr Thr
96      210      215      220
99 Leu Gly His Arg Asn Pro Gln Gly Leu Ala Phe Ala Pro Asn Gly Lys
100 225      230      235      240
103 Leu Leu Gln Ser Glu Gln Gly Pro Asn Ser Asp Asp Glu Ile Asn Leu
104      245      250      255
107 Val Leu Lys Gly Gly Asn Tyr Gly Trp Pro Asn Val Ala Gly Tyr Lys
108      260      265      270
111 Asp Asp Ser Gly Tyr Ala Tyr Ala Asn Tyr Ser Ala Ala Thr Asn Lys
112      275      280      285
115 Ser Gln Ile Lys Asp Leu Ala Gln Asn Gly Ile Lys Val Ala Thr Gly
116      290      295      300
119 Val Pro Val Thr Lys Glu Ser Glu Trp Thr Gly Lys Asn Phe Val Pro
120 305      310      315      320
123 Pro Leu Lys Thr Leu Tyr Thr Val Gln Asp Thr Tyr Asn Tyr Asn Asp
124      325      330      335
127 Pro Thr Cys Gly Glu Met Ala Tyr Ile Cys Trp Pro Thr Val Ala Pro
128      340      345      350
131 Ser Ser Ala Tyr Val Tyr Thr Gly Lys Lys Ala Ile Pro Gly Trp
132      355      360      365
135 Glu Asn Thr Leu Leu Val Pro Ser Leu Lys Arg Gly Val Ile Phe Arg
136      370      375      380
139 Ile Lys Leu Asp Pro Thr Tyr Ser Thr Thr Leu Asp Asp Ala Ile Pro
140 385      390      395      400
143 Met Phe Lys Ser Asn Asn Arg Tyr Arg Asp Val Ile Ala Ser Pro Glu
144      405      410      415
147 Gly Asn Thr Leu Tyr Val Leu Thr Asp Thr Ala Gly Asn Val Gln Lys
148      420      425      430
151 Asp Asp Gly Ser Val Thr His Thr Leu Glu Asn Pro Gly Ser Leu Ile
152      435      440      445
155 Lys Phe Thr Tyr Asn Gly Lys
156      450      455
159 <210> SEQ ID NO: 2
160 <211> LENGTH: 1368
161 <212> TYPE: DNA
162 <213> ORGANISM: Acinetobacter baumannii
164 <400> SEQUENCE: 2

```

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DATE: 03/22/2006

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TIME: 14:56:03

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

```

165 gatatacctc tgacacctgc tcagttcgca aaagcgaaaa cagaaaatTT tgataaaaaa      60
167 gtgattctgt ccaattttaa taaaccacat gctttgttat gggggccaga taatcaaatt      120
169 tggttaaccg aacgtgcaac tggcaaaatt ttaagagtaa atcctgtatc tggtagcgcg      180
171 aaaacagtat ttcaggttcc tgaaattgtg agtgatgctg atgggcaaaa tggtttgTTa      240
173 ggttttgcTT ttcacTctga ctttaaacaT aacccttata tctatatttc aggcactttt      300
175 aaaaatccaa aatctacaga taaagagtta cctaatacaga cgattattcg tagatatacc      360
177 tataataaaa ctacagatac atttgaaaag cctattgatt tgattgcagg tttaccgtca      420
179 tcaaaagatc atcagTctgg tCgtctcgTT attggTccag accaaaaaaT ctactatacg      480
181 attggtgacc aaggTcgtaa tcagTtagct tatctgttct taccgaatca ggcacagcat      540
183 actccgactc agcaagagct caatagtaaa gactaccata catatatggg taaagtatta      600
185 cgcttaaattc tggacggcag tgtacctaTaa gacaacccaa gctttaacgg cgtagtgagt      660
187 catatctaca ctttagggca ccgtaatcca caaggTttag catttgcccc aaatggaaag      720
189 cttttacaat ctgagcaagg accaaattct gatgatgaaa ttaaccttgt attaaaaggT      780
191 ggtaactatg gctggccaaa tgtagctggT tataaagatg acagtggTTa tgcctatgca      840
193 aactattcgg cagcaaccaa taaatcacia attaaagatt tagctcaaaa cgggataaaa      900
195 gtagcaacag gtgttctctg gactaaagag tctgaatgga ctggtaaaaa ctttTgtgccg      960
197 ctttgaaaa ctttatatac ggtacaagat acctataact ataatgaccc tacttTgtggT      1020
199 gagatggcat atattTgtcg gccaacggTt gcaccgtcat cagcatatgt atatacggga      1080
201 ggcaaaaaag cgattccagg gtgggaaaaT acattattgg tcccatcttt aaaacgtggg      1140
203 gtgattttcc gtattaaatt ggaccgcaga tatagcacga ctttggatga tgctatccca      1200
205 atgttttaaaa gcaataaccg ttatcgTgat gTcatcgcta gtccagaagg taatacctta      1260
207 tatgtgctga ctgatacagc ggggaatgta caaaaagatg atggttctgt cactcatact      1320
209 ttagagaatc ccggttctct cattaaattt acatataacg gtaagtaa      1368
212 <210> SEQ ID NO: 3
213 <211> LENGTH: 33
214 <212> TYPE: DNA
215 <213> ORGANISM: Artificial
217 <220> FEATURE:
218 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
220 <400> SEQUENCE: 3
221 agtgatgctg atgggaataa tggtttgTTa ggt      33
224 <210> SEQ ID NO: 4
225 <211> LENGTH: 33
226 <212> TYPE: DNA
227 <213> ORGANISM: Artificial
229 <220> FEATURE:
230 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
232 <400> SEQUENCE: 4
233 agtgatgctg atggggagaa tggtttgTTa ggt      33
236 <210> SEQ ID NO: 5
237 <211> LENGTH: 33
238 <212> TYPE: DNA
239 <213> ORGANISM: Artificial
241 <220> FEATURE:
242 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
244 <400> SEQUENCE: 5
245 agtgatgctg atgggacaaa tggtttgTTa ggt      33
248 <210> SEQ ID NO: 6
249 <211> LENGTH: 33

```

## RAW SEQUENCE LISTING

DATE: 03/22/2006

PATENT APPLICATION: US/10/570,904

TIME: 14:56:03

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

```

250 <212> TYPE: DNA
251 <213> ORGANISM: Artificial
253 <220> FEATURE:
254 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
256 <400> SEQUENCE: 6
257 agtgatgctg atgggatgaa tggtttgta ggt 33
260 <210> SEQ ID NO: 7
261 <211> LENGTH: 33
262 <212> TYPE: DNA
263 <213> ORGANISM: Artificial
265 <220> FEATURE:
266 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
268 <400> SEQUENCE: 7
269 agtgatgctg atggggggaa tggtttgta ggt 33
272 <210> SEQ ID NO: 8
273 <211> LENGTH: 33
274 <212> TYPE: DNA
275 <213> ORGANISM: Artificial
277 <220> FEATURE:
278 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
280 <400> SEQUENCE: 8
281 agtgatgctg atgggaagaa tggtttgta ggt 33
284 <210> SEQ ID NO: 9
285 <211> LENGTH: 33
286 <212> TYPE: DNA
287 <213> ORGANISM: Artificial
289 <220> FEATURE:
290 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
292 <400> SEQUENCE: 9
293 gaccaaggctc gtaatatatt agcttatctg ttc 33
296 <210> SEQ ID NO: 10
297 <211> LENGTH: 33
298 <212> TYPE: DNA
299 <213> ORGANISM: Artificial
301 <220> FEATURE:
302 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
304 <400> SEQUENCE: 10
305 gaccaaggctc gtaatgtatt agcttatctg ttc 33
308 <210> SEQ ID NO: 11
309 <211> LENGTH: 33
310 <212> TYPE: DNA
311 <213> ORGANISM: Artificial
313 <220> FEATURE:
314 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
316 <400> SEQUENCE: 11
317 gaccaaggctc gtaatgcatt agcttatctg ttc 33
320 <210> SEQ ID NO: 12
321 <211> LENGTH: 43
322 <212> TYPE: DNA

```

## RAW SEQUENCE LISTING

DATE: 03/22/2006

PATENT APPLICATION: US/10/570,904

TIME: 14:56:03

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

```

323 <213> ORGANISM: Artificial
325 <220> FEATURE:
326 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
328 <400> SEQUENCE: 12
329 cgaatcaggc acagcatact ccgactcagc aagagctcaa tag          43
332 <210> SEQ ID NO: 13
333 <211> LENGTH: 45
334 <212> TYPE: DNA
335 <213> ORGANISM: Artificial
337 <220> FEATURE:
338 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
340 <220> FEATURE:
341 <221> NAME/KEY: misc_feature
342 <222> LOCATION: (17)..(25)
343 <223> OTHER INFORMATION: n stands for any base
346 <400> SEQUENCE: 13
W--> 347 gtaagaacag ataagcnnnn nnnnnacgac cttggtcacc aatcg      45
350 <210> SEQ ID NO: 14
351 <211> LENGTH: 40
352 <212> TYPE: DNA
353 <213> ORGANISM: Artificial
355 <220> FEATURE:
356 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
358 <400> SEQUENCE: 14
359 gatgctgatg ggcaaaatgg tttgttaggt tttgcttttc          40
362 <210> SEQ ID NO: 15
363 <211> LENGTH: 38
364 <212> TYPE: DNA
365 <213> ORGANISM: Artificial
367 <220> FEATURE:
368 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
370 <220> FEATURE:
371 <221> NAME/KEY: misc_feature
372 <222> LOCATION: (7)..(15)
373 <223> OTHER INFORMATION:
375 <220> FEATURE:
376 <221> NAME/KEY: misc_feature
377 <222> LOCATION: (7)..(15)
378 <223> OTHER INFORMATION: n stands for any base
W--> 381 <400> 15
W--> 382 actcacnnnn nnnnnaacct gaaatactgt tttcgcg      38
385 <210> SEQ ID NO: 16
386 <211> LENGTH: 50
387 <212> TYPE: DNA
388 <213> ORGANISM: Artificial
390 <220> FEATURE:
391 <223> OTHER INFORMATION: Artificial Sequence oligonucleotide
393 <400> SEQUENCE: 16
394 tttaccgtca tcaaaagatc atcagtctgg tcgtctcggt attggtccag      50

```

<210> 73  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Artificial Sequence oligonucleotide

<400> 73  
 ggcataatatt tgctggccan~~nn~~gttgcacc gtcatacgc

39

← pls explain "N" locations.

<210> 74  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <223> Artificial Sequence oligonucleotide

<400> 74  
 gctgactgat acagcggggn~~nn~~gtacaaaa agatgatgg

39

← pls explain "N" locations,

← See error explanation on  
 page 9.



&lt;210&gt; 87

&lt;211&gt; 38

&lt;212&gt; DNA

&lt;213&gt; The sequence of designed polynucleotide described as seq87

polynucleotide

&lt;400&gt; 87

gcttttataaa tctgaccaag gaccaaattc tgatgatg

Invalid  
Response

38

&lt;210&gt; 88

&lt;211&gt; 39

&lt;212&gt; DNA

&lt;213&gt; synthetic DNA

Invalid  
Response

&lt;400&gt; 88

gaccaaggct gtaatgcgtt agcttatctg ttcttaccg

39

See item # 11 on error  
Summary sheet.F Y I:<213> responses has to be  
either Artificial,  
Unknown or genus/species.The type of errors shown exist throughout  
the Sequence Listing. Please check subsequent  
sequences for similar errors.

RAW SEQUENCE LISTING ERROR SUMMARY  
PATENT APPLICATION: US/10/570,904

DATE: 03/22/2006  
TIME: 14:56:04

Input Set : A:\251134.st25 - Sequence Listing.txt  
Output Set: N:\CRF4\03222006\J570904.raw

**Please Note:**

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:13; N Pos. 17,18,19,20,21,22,23,24,25 ✓

Seq#:15; N Pos. 7,8,9,10,11,12,13,14,15 ✓

Seq#:17; N Pos. 18,19,20,21,22,23,24,25,26 ✓

Seq#:19; N Pos. 16,17,18,19,20,21,22,23,24 ✓

Seq#:21; N Pos. 17,18,19

Seq#:30; N Pos. 16

Seq#:33; N Pos. 16

Seq#:34; N Pos. 16

Seq#:49; N Pos. 17

Seq#:58; N Pos. 17

Seq#:60; N Pos. 17

Seq#:61; N Pos. 17

Seq#:62; N Pos. 17

Seq#:63; N Pos. 17

Seq#:69; N Pos. 19,20

Seq#:70; N Pos. 19,20

Seq#:71; N Pos. 19,20

Seq#:73; N Pos. 20,21,22

Seq#:74; N Pos. 20,21,22

**Invalid <213> Response:**

Use of "Artificial" only as "<213> Organism" response is incomplete,  
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,26,27,28,29

Seq#:30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53

Seq#:54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74

## VARIABLE LOCATION SUMMARY

DATE: 03/22/2006

PATENT APPLICATION: US/10/570,904

TIME: 14:56:04

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

Use of n's or Xaa's (NEW RULES):

*Error Explanation: Ⓢ*

Use of n's and/or Xaa's have been detected in the Sequence Listing.

Use of &lt;220&gt; to &lt;223&gt; is MANDATORY if n's or Xaa's are present.

in <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.

Seq#:13; N Pos. 17,18,19,20,21,22,23,24,25

Seq#:15; N Pos. 7,8,9,10,11,12,13,14,15

Seq#:17; N Pos. 18,19,20,21,22,23,24,25,26

Seq#:19; N Pos. 16,17,18,19,20,21,22,23,24

Seq#:21; N Pos. 17,18,19

Seq#:30; N Pos. 16

Seq#:33; N Pos. 16

Seq#:34; N Pos. 16

Seq#:49; N Pos. 17

Seq#:58; N Pos. 17

Seq#:60; N Pos. 17

Seq#:61; N Pos. 17

Seq#:62; N Pos. 17

Seq#:63; N Pos. 17

Seq#:69; N Pos. 19,20

Seq#:70; N Pos. 19,20

Seq#:71; N Pos. 19,20

Seq#:73; N Pos. 20,21,22

Seq#:74; N Pos. 20,21,22

## VERIFICATION SUMMARY

DATE: 03/22/2006

PATENT APPLICATION: US/10/570,904

TIME: 14:56:04

Input Set : A:\251134.st25 - Sequence Listing.txt

Output Set: N:\CRF4\03222006\J570904.raw

L:14 M:270 C: Current Application Number differs, Replaced Current Application No  
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:347 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0  
L:381 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:15,Line#:373  
L:382 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15 after pos.:0  
L:412 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17 after pos.:0  
L:442 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0  
L:472 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21 after pos.:0  
L:586 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:30 after pos.:0  
L:628 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:33 after pos.:0  
L:646 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:34 after pos.:0  
L:832 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:49 after pos.:0  
L:946 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:58 after pos.:0  
L:976 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:60 after pos.:0  
L:994 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:61 after pos.:0  
L:1012 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:62 after pos.:0  
L:1030 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:63 after pos.:0  
L:1108 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:69 after pos.:0  
L:1126 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:70 after pos.:0  
L:1144 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:71 after pos.:0  
L:1168 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:73  
L:1168 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:73  
L:1168 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:73 after pos.:0  
L:1180 M:258 W: Mandatory Feature missing, <221> Tag not found for SEQ ID#:74  
L:1180 M:258 W: Mandatory Feature missing, <222> Tag not found for SEQ ID#:74  
L:1180 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:74 after pos.:0